

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
CO, Man S.

(ii) TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF
MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR
PREVENTION OF ACUTE ORGAN DAMAGE AFTER
EXTRACORPOREAL BLOOD CIRCULATION

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Felfe & Lynch
(B) STREET: 805 Third Avenue
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 10022

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" Computer Disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII, WordPerfect 5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/578,953
(B) FILING DATE: 27-Dec-95
(C) CLASSIFICATION: 530

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: EP 95 112 895.8
(B) FILING DATE: 17-Aug-95
(A) APPLICATION NUMBER: EP 95 114 969.9
(B) FILING DATE: 19-Sep-95

(viii) ATTORNEY/AGENT INFORMATION

(A) NAME: Hanson, Norman D.
(B) REGISTRATION NUMBER: 30,946
(C) REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH

(ix) TELECOMMUNICATION INFORMATION

(A) TELEPHONE: (212) 688-9200
(B) TELEFAX: (212) 838-3884

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1,,654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GAC	ATT	CAG	ATG	ACC	CAA	TCT	CCG	AGC	TCT	TTG	TCT	GCG	TCT	GTA	GGG	48
Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1				5					10					15		
GAT	AGG	GTC	ACT	ATC	ACC	TGC	AAG	GCC	AGC	CAA	AGT	GTT	GAT	TAT	GAT	96
Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Ser	Val	Asp	Tyr	Asp	
			20					25					30			
GGT	GAT	AGT	TAT	ATG	AAC	TGG	TAC	CAA	CAG	AAA	CCA	GGA	AAG	GCA	CCC	144
Gly	Asp	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	
		35				40						45				
AAG	CTT	CTC	ATC	TAT	GCT	GCA	TCC	AAC	CTA	GAA	TCT	GGT	ATC	CCA	TCC	192
Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Ile	Pro	Ser	
	50					55					60					
AGG	TTT	AGT	GGC	AGT	GGG	TCT	GGG	ACA	GAC	TTC	ACC	CTC	ACC	ATC	TCT	240
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	
65					70				75					80		
TCT	CTG	CAG	CCG	GAG	GAT	TTC	GCA	ACC	TAT	TAC	TGT	CAG	CAA	AGT	AAT	288
Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Asn	
			85					90						95		
GAA	GAT	CCG	TGG	ACG	TTC	GGT	CAA	GGC	ACC	AAG	GTG	GAA	ATC	AAA	CGA	336
Glu	Asp	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	
		100						105					110			
ACT	GTG	GCT	GCA	CCA	TCT	GTC	TTC	ATC	TTC	CCG	CCA	TCT	GAT	GAG	CAG	384
Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	
		115						120					125			
TTG	AAA	TCT	GGA	ACT	GCC	TCT	GTT	GTG	TGC	CTG	CTG	AAT	AAC	TTC	TAT	432
Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	
	130					135						140				

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CCC	AGA	GAG	GCC	AAA	GTA	CAG	TGG	AAG	GTG	GAT	AAC	GCC	CTC	CAA	TCG	480
Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	
145					150					155					160	
GGT	AAC	TCC	CAG	GAG	AGT	GTC	ACA	GAG	CAG	GAC	AGC	AAG	GAC	AGC	ACC	528
Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	
			165						170					175		
TAC	AGC	CTC	AGC	AGC	ACC	CTG	ACG	CTG	AGC	AAA	GCA	GAC	TAC	GAG	AAA	576
Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	
			180					185						190		
CAC	AAA	GTC	TAC	GCC	TGC	GAA	GTC	ACC	CAT	CAG	GGC	CTG	AGC	TCG	CCC	624
His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	
		195					200					205				
GTC	ACA	AAG	AGC	TTC	AAC	AGG	GGA	GAG	TGT							654
Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys							
	210					215										

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1				5					10					15		
Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Ser	Val	Asp	Tyr	Asp	
		20					25						30			
Gly	Asp	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	
		35				40						45				
Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Ile	Pro	Ser	
	50				55					60						
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	
65				70				75						80		
Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Asn	
			85					90						95		
Glu	Asp	Pro	Trp	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	
		100				105							110			

Sequence = TGGTGG

TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAG	GAA	GAC	CCC	GAG	GTC	CAG	TTC	AAC	816
Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	
			260					265					270			
TGG	TAC	GTG	GAT	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	CGG	864
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	
		275					280					285				
GAG	GAG	CAG	TTC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC	GTC	CTC	ACC	GTC	912
Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	
		290				295					300					
CTG	CAC	CAG	GAC	TGG	CTG	AAC	GGC	AAG	GAG	TAC	AAG	TGC	AAG	GTC	TCC	960
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	
					310					315					320	
AAC	AAA	GGC	CTC	CCG	TCC	TCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA	1008
Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	
				325					330					335		
GGG	CAG	CCC	CGA	GAG	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CAG	GAG	1056
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	
			340					345					350			
GAG	ATG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	1104
Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	
		355					360					365				
TAC	CCC	AGC	GAC	ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	1152
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	
		370				375					380					
AAC	AAC	TAC	AAG	ACC	ACG	CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	1200
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	
					390					395					400	
TTC	CTC	TAC	AGC	AGG	CTA	ACC	GTG	GAC	AAG	AGC	AGG	TGG	CAG	GAG	GGG	1248
Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	
				405				410						415		
AAT	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC	TAC	1296
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	
			420				425					430				
ACA	CAG	AAG	AGC	CTC	TCC	CTG	TCT	CTG	GGT	AAA						1329
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys						
		435				440										

Sequence 1

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443
- (B) TYPE: amino acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Ser Ile Ser Thr Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys
50 55 60
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Arg Asp Tyr Asp Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115 120 125
Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
130 135 140
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
180 185 190
Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
195 200 205
Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser
210 215 220

Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 225 230 235 240
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 245 250 255
 Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
 260 265 270
 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 275 280 285
 Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 290 295 300
 Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 305 310 315 320
 Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
 325 330 335
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
 340 345 350
 Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 355 360 365
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 370 375 380
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 385 390 395 400
 Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
 405 410 415
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 420 425 430
 Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 435 440

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acid residues
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

